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AACTGGGANG AAGGGCGCAC CCTGGCAGAT TNCNACATTC CNAAAGAATC CACCTTCACC 600
 TGGTGCTCCC CCTCCGCCGG GGTCCCTAAC CCTTTTGGGC TGTATGTNTC CCCTGCCTTT 660
 5 GCTGTCTTAA TTCNCTCTGT TGGTGTTTCGT TGGAAATTCC CTAATCCNGA AGGTTCTTNA 720
 AAAGGAAATN AANCCNNTTG GGTTCCTCCC TTTGGCCTTT TTTTGTGTTG AAAATCCTNT 780
 GTTTTTGGTG T 791

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: U-U120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

GGCACNANCC CGCTTCGGTA GCCATTATTG GTGCCCGTAG AGCGAGTGCT GAGATGGCTT 60
 TGAGGGCCTT CTCCCCCTC TGCATCGCTC TCGTGGTGAC GCTCTCACCT CTGTGTGATG 120
 CCACTTCGCC TTACTACACC ATCACACCGC CCACCCCGT GGCCAAGCCG CCTTCAGTTG 180
 35 AACCACCACC CTACCACGGC CCTCCGACNA CCCACCCTAA GCCACCGAGT CATGGTGGCC 240
 AACCTCCGTC CCACCATCAC CCAACACCAA TCTACGGTGC ACCCCCTCCG CAACACCACC 300
 ACCACCACCA ACACCACCAC CAACCTGCAC CACCAACTCA CGCANAAACAC CCTCCGTACT 360
 40 ACCACATGCC TTCCCCGCCG CCGCATGGCC AGCACCCGTC ACCACCGTCA CATGATTATC 420
 CCGTACCTCC TGCTCACAAG CCCCAGACTC CGCCGCCGGT TTACAAGTCT CCACCACCGA 480
 45 NCCACCGTCC TTACCCTCCA TCGACGCCAC CCCACCATCC GAAGCACCCG CCTTCTCAGC 540
 CGAAGCCGTC NTACAAGGCC CGCCACCATN CAAGAACATC CCTGANCACT CTCCACCGCC 600
 GCGTCACTAT CATTCTCCGT CTTACCACCC ACCACCACCA CCATACAAAA TAATCTCGTT 660
 50 TTGCCATCTT CTCCCGTTTG AAAAAAANN CAANTGTCCT TTTTATTAA CCNAATCCAN 720
 GGGGTTTTTN TTAANATTN AANAAANCNA ANTNTTTTCC CCCCNTNTT GGTNATGGC 780
 55 CTATGGGTTT GTTCTCTTC TTGGCTTTTC CCGG 814

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 742 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: U-U126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

5 GGCACGAGGT TGTGCCTAAC AGAGAGAGAG AGAGACAGAC CGATAGCCTC CTCATTCACT 60
ATGGCGATCC GATCGCCAGC TTCGCTGCTG TTATTTGCGT TTCTGATGCT TGCCTCACA 120
GGAAGACTGC AGGCCGGGCG CAGCTCATGC ATTGGCGTCT ACTGGGGACA AAACACAGAC 180
10 GAGGGAAGCT TAGCAGATGC TTGTGCCACA GGCAACTACG AATACGTGAA CATCGCCACC 240
CTTTTCAAGT TTGGCATGGG CCAAACCTCA NANATCAACC TCGCCGGCCA CTGTGACCCT 300
CGGAACAACG GCTGCGCGCG CTTAAGCAGC GAAATCCAGT CCTGCCAGGA GCGTGGAGTC 360
15 AAGGTGATGC TCTCCATCGG AGGTGGCGGG TCTTATGGCC TGAGTTCCAC CGAANACGCC 420
AAGGACGTGG CGTCATACCT CTGGCACAGT TTCTTGGGTG GTTCTGCTGC TCGCTACTCT 480
20 CNACCCCTCG GGGATGCGGT TCTGGATGGC ATANACTTCA ACATCCCCGG AGGGAGCACA 540
GAACACTATG ATGAACTTGC CGCTTTCCTC CNAGGGCTAC AACGAACAGG AAGCCGGAAC 600
CAAAAAAGTT TCACTTGAAT TGCTGCTCCC NCANTGTCTT TTCCCGATT ACTGGCTTTG 660
25 GCAACCCACT CCAAAACAAA TNTCTTCNA CTTCCNTGTT GGGTTGCNAA NTTCCNTTCC 720
CAANCAAACC CCTTTCNTTT GC 742

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 794 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

GGCACGAGGG CGTGGCGGAG ATGGGGAGCT GGCGGGCTCT GTTGCAGCGG CGGCTGCTGT 60
50 TGCTCTCTGC TTTGGCGGTG GCTGTTCGTG TGAAGGCACT CAGCANANAC NATTTCCCGG 120
COGGCTTCAT TTTTGGCGCA GGCACCTCCG CTTATCAGGT ANAAGGTGCA GCTGCAGAGG 180
55 GGGGAANAAC ACCCAGCATT TGGGACACGT TTACGCATGC AGGGAGAACT TTCGACCAGA 240
GCACCGGAGA CGTAGCAGCT GATCAGTATC ACAAGTACAA GGAAGATGTG AANCTGATGC 300
ATGANATGGG CTTGATGCT TACAGATTCT CCATCTCCTG GTCCANAGTT ATCCCCAATG 360
60 GTCGAGGGCC TGTGAATCCA CAAGGCTTGC GGTACTACAA CAACCTGATC GATGAGCTCN 420
AAAGATATGG AATCCGAGCC TCATGTCACT CTTTACCACT TCGACCTTCC GCAAGCACTG 480
65 GAANACGAAT NCGCCGGGCA GCTGAACCCA AAGATCGTAN ANGAATTAC CGCTTACGCC 540
AACGTTTTGC TTCANCNAAT TTGGGGATCN AATCTAGCAC TGGATCNCCT ATCAATGAAC 600
CAACATANAT CCCGTCCTCC GCCACNAATT CCGCATCTTC NCCCCTGGCC CCTGCTCTTT 660
70 ATCCCTTNCG CCTCCAACCTG CNCCAAGGGC NACTCCCCC CATTTTNAAN CCCATNNNNT 720

CCNCCCCCCC CAATTAACCC NTTCTTGCTC TTCCCCCTTG CCTTCANCCA ACCCGCCCN 780
TTTCCNAAAA AANA 794

5 (2) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 799 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U130

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

GGCACGAGCC GGCCTCAGGC ATATGGTGCG GTCGCTACAC GTGTCAGGC AAGGCCGGGA 60
GCCGCGCAGG ATCATCAGGG AAGCACTGTC GAAGGCGCTG GTGAAGTACT ACCCCTTCGC 120
GGGGCGGTTC GTGGACNATC CCGAGGGCGG CGGCGAGGTT CGTGTGCTT GCACTGGCGA 180
GGGCGCTTGG TTCGTCNAGG CCAAGGCGGA CTGCAGCTTG GAGGACGTGA AGTACCTCGA 240
TCTCCCGCTC ATGATCCCTG AGGACGCGCT CCTGCCAAG CCCTGCCCCG GACTGAACCC 300
CCTCGACCTC CCTCTCATGC TGCAGGTGAC ANANTTCGTG GGCGGCGGAT TCGTGGTCGG 360
CCTCATCTCC GTCCATACCA TCGCCGACGG CCTCGGCGTC NTCCANTTCA TCAACGCCGT 420
CGCCCCGAAAT CGCCCGTGGC CTGCCNAANC CCACCGTGGA NCCTGCATGG TCCCGGGANG 480
TCNTACCCAA CCCACCTAAG CTGCCTCCCG GTGGCCCGCC CGTGTTCCTC CTCCTTCAAN 540
CTGCTCCACG CCACCGTCGA ACTATCCCCT GACCACATCC ATCAGTCAA GTCCCCACAC 600
TTTGGANCTC ACCCGGCCAA CGTGCTCTA CCTTCCACNT CCCCATCCCC AACCTGTTTG 660
NAATCCGCA CGCCCCGCN TCNACCTTGG AACCCAAGGC NTTTCCAANC TTTGCAACCC 720
TTTTTTCCTT TCCTTCCCCC CCAAAANAA CTCCCCCA CCCTTGTTT TGCNCCAAG 780
TTTTTTCCTT CCTTGCCCC 799

50 (2) INFORMATION FOR SEQ ID NO: 33:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 759 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U43

65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

GGAGGTTGTT GTTCATGTCC CTAATTCGGG GTCTCCTGTA CAGATTGAAT TTCAAGTAAC 60
TAATAGCAGT GGCTACTTGG TGCTTCATTG GGGTGCAATT CATAATAGAA GGAATAACTG 120